

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shak, Steven
- (ii) TITLE OF INVENTION: Anti-Infective Therapy
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: 07-Nov-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/669306
 - (B) FILING DATE: 25-Sep-2001
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/873506
 - (B) FILING DATE: 08-Dec-1999
- (ix) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/643195
 - (B) FILING DATE: 06-May-1996
- (x) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/459909
 - (B) FILING DATE: 02-Jun-1995
- (xi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/191749
(B) FILING DATE: 03-Feb-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/914,226
(B) FILING DATE: 13-Jul-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/448038
(B) FILING DATE: 08-Dec-1989

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/289958
(B) FILING DATE: 23-Dec-1988

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Johnston, Sean A.
(B) REGISTRATION NUMBER: 35,910
(C) REFERENCE/DOCKET NUMBER: P0530P1C10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-3562
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTGGACA CCTACCAAGTA TGATGATGGC TGTGAGTCCT GTGGCAATGA 50

C 51

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
1 5 10 15

Asn Asp

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TATGACGTCT ACCTGGACGT GCAGCAGAAG TGGCATCTGA ATGATGTGAT 50
GCTGATGGGC GACTTCAACG C 71

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
1 5 10 15

Val Met Leu Met Gly Asp Phe Asn
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CC 42

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCGCATGTC CCAGGGCCAC AGGCAGCGTT TCCTGGTAGG AC 42

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGAAGATCG CAGCCTTCAA CATCCAGACA T 31

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGGATGTTG AAGGVTGCGA TCTTCAATGC A 31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGAATTAT GTTAAAAATT GCAGCATTAA ATATTCAAAC AT 42

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGAATATTA AATGCTGCAA TTTTAACAT AATT 34

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Lys Ile Ala Ala Phe
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1039 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCTGCACAG GCAGTGCCTT GAAGTGCTTC TTCAGAGACC TTTCTTCATA 50

GACTXACTTTT TTTTCTTTAA GCAGCAAAAG GAGAAAATTG TCATCAAAGG 100
ATATTCCAGA TTCTTGACAG CATTCTCGTC ATCTCTGAGG ACATCACCAT 150
CATCTCAGGA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC 200
GCCCTACTG CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC 250
AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 300
GTGCAGATCC TGAGCCGCTA TGACATCGCC CTGGTCCAGG AGGTCAAGAGA 350
CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAAACCTC AATCAGGATG 400
CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC 450
TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT 500
GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT 550
TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 600
AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC 650
CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG 700
GCTTGGAGGA CGTCATGTTG ATGGCGACT TCAATGCGGG CTGCAGCTAT 750
GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT 800
CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT 850
GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGCGCCGTT 900
GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG 950
TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC 1000
TGAAGTGAGC AGCCCCCTCCC CACACCAGTT GAACTGCAG 1039

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser Cys Thr Gly Ser Ala Leu Lys Cys Phe Phe Arg Asp Leu Ser
 1 5 10 15

Ser Thr Thr Phe Phe Ser Leu Ser Ser Lys Arg Arg Lys Leu Ser
 20 25 30

Ser Lys Asp Ile Pro Asp Ser Gln His Ser Arg His Leu Gly His
 35 40 45

His His His Leu Arg Met Arg Gly Met Lys Leu Leu Gly Ala Leu
 50 55 60

Leu Ala Leu Ala Ala Leu Leu Gln Gly Ala Val Ser Leu Lys Ile
 65 70 75

Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser Asn
 80 85 90

Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp
 95 100 105

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
 110 115 120

Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr
 125 130 135

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu
 140 145 150

Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp
 155 160 165

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr
 170 175 180

Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr
 185 190 195

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
 200 205 210

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp
 215 220 225

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp
 230 235 240

Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser
 245 250 255

Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp
 260 265 270

Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg
 275 280 285

Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp
 290 295 300

Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp
 305 310 315

Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val Met
 320 325 330

Leu Lys Ala Ala Pro Pro His Thr Ser Thr Ala
 335 340

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
 1 5 10 15

Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser
 20 25 30

Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu
 35 40 45

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro
 50 55 60

Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
 65 70 75

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
 80 85 90

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly
 95 100 105

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser
 110 115 120

Arg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala
 125 130 135

Ala Pro Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val
 140 145 150

Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu
 155 160 165

Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
 170 175 180

Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu
 185 190 195

Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala
 200 205 210

Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val
 215 220 225

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
 230 235 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
 245 250 255

Glu Val Met Leu Lys
 260

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Lys Ile Ala Ala Phe Asn Ile Arg Thr Phe Gly Glu Thr Lys
 1 5 10 15

Met Ser Asn Ala Thr Leu Ala Ser Tyr Ile Val Arg Ile Val Arg
 20 25 30

Arg Tyr Asp Ile Val Leu Ile Glu Gln Val Arg Asp Ser His Leu
 35 40 45

Val Ala Val Gly Lys Leu Leu Asp Tyr Leu Asn Gln Asp Asp Pro
 50 55 60

Asn Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
 65 70 75

Tyr Lys Glu Arg Tyr Leu Phe Leu Phe Arg Pro Asn Lys Val Ser
 80 85 90

Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
 95 100 105

Asn Asp Ser Phe Ser Arg Glu Pro Ala Val Val Lys Phe Ser Ser
 110 115 120

His Ser Thr Lys Val Lys Glu Phe Ala Ile Val Ala Leu His Ser
 125 130 135

Ala Pro Ser Asp Ala Val Ala Glu Ile Asn Ser Leu Tyr Asp Val
 140 145 150

Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp Val Met Leu
 155 160 165

Met Gly Asp Phe Asn Ala Asp Cys Ser Tyr Val Thr Ser Ser Gln
 170 175 180

Trp Ser Ser Ile Arg Leu Arg Thr Ser Ser Thr Phe Gln Trp Leu
 185 190 195

Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Ser Thr Asn Cys Ala

(2) INFORMATION FOR SEO ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCCCT AACTCCGCC C ATCCCGCCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG 300
CAGAGGCCGA GGCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTG GAGGCCTAGG CTTTGCAAA AAGCTTATCG GGCCGGGAAC 400
GGTGCATTGG AACGCGGATT CCCC GTGCCA AGAGTGACGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTATGTA TCATACACAT ACGATTTAGG TGACACTATA 550

GAATAACATC CACTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600
AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTGCGCCGT GAATTAAAGG 650
GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 664 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCCCT AACTCCGCC ATCCCGCCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTATG 300
CAGAGGCCGA GGCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTG GAGGCCTAGG CTTTGCAAA AAGCTTATCC GGCGGGAAC 400
GGTGCATTGG AACGCGGATT CCCC GTGCCA AGAGTCAGGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTATGTA TCATACACAT ACGATTAGG TGACACTATA 550
GAATAACATC CACTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC 600
AACTGCACCT CGGTTCTAAG CTTGGGCTGC AGGTGCCCCGT GAATTAAAGG 650
GACGCTGTGA AGCA 664

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGAAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG 300
CAGAGGCCGA GGCGGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTG GAGGCCTAGG CTTTGCAAA AAGCTTATCC GGCGGGAAC 400
GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTTGGA TCCTATAGAC TGACATCCAC TTTGCCTTTC 550
TCTCCACAGG TGTCCACTCC CAGGTCCAAC TGCACCTCGG TTCGAAGCTT 600
GGGCTGCAGG TCGCCGTGAA TTTAAGGGAC GCTGTGAAGC 640

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCCC TAACTCCGCC 250
CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT TTTATTATG 300
CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTG GAGGCCTAGG CTTTGCAAA AAGCTTATCC GGCCGGGAAC 400
GGTGCATTGG AACGCGGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTTGGA TCCTACTAAC TACTGACTTA TTCTTTCCCT 550
TTCTCTCCAC AGGTGTCCAC TCCCAGGTCC AACTGCACCT CGGTTCGCGA 600
AGCTTGGGCT GCAGGTGCGCC GTGAATTAA GGGACGCTGT GAAGCA 646

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGACA GCTGTGGAAT 50
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG 100
TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC 150
CAGGCTCCCC AGCAGGCAGA AGTATGCAA GCATGCATCT CAATTAGTCA 200
GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCCC TAACTCCGCC 250

CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG 300
CAGAGGCCGA GGCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA 350
GGCTTTTTG GAGGCCTAGG CTTTGCAAA AAGCTTATCC GGCGGGAAC 400
GGTGCATTGG AACGC GGATT CCCCGTGCCA AGAGTCAGGT AAGTACCGCC 450
TATAGAGTCT ATAGGCCAC CCCCTGGCT TCGTTAGAAC GCGGCTACAA 500
TTAATACATA ACCTTTGGA TCCTACTGAC ACTGACATCC ACTTTTCTT 550
TTTCTCCACA GGTGTCCACT CCCAGGTCCA ACTGCACCTC GGTCGCGAA 600
GCTTGGGCTG CAGGTCGCCG TGAATTAAAG GGACGCTGTG AAGCA 645

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGACGTAAGT ACATGTATCA TACACATACG ATTTAGGTGA CACTATAGAA 50

TAACATCCAC TTTGCCTTTC TCTCCACAGG T 81

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCAGGTAAGT ACATGTATCA TACACATACG ATTTAGGTGA CACTATAGAA 50

TAACATCCAC TTTGCCTTTC TCTCCACAGG T 81

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCAGGTAAGT ACTTGGATCC TATAGACTGA CATCCACTTT GCCTTTCTCT 50

CCACAGGT 58

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCAGGTAAGT ACTTGGATCC TACTAACTAC TGACTTATTC TTTTCCTTTC 50

TCTCCACAGG T 61

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCAGGTAAGT ACTTGGATCC TACTGACACT GACATCCACT TTTTCTTTT 50

CTCCACAGGT 60